AMENDMENTS TO THE SPECIFICATION

At page 8, please replace the paragraph at lines 13-32 with the following:

The human eNOS gene provides a series of polymorphisms, in which a single base is exchanged (SNP stands for single nucleotide polymorphism) also, for example, a T to C transition in the promoter of the gene at position -786 (FIG. 1). Linkage analyses show that this base exchange does not occur in isolation, but is always associated with an A to G transition at position -922 and a T to A transition at position -1486. The functional significance of these polymorphisms is so far unknown, with the exception of the T to C transition at position -786, which has now been explained by the inventors, (Wattanapitayakul et al. ~~(2000)~~2001 Trends Pharmacol. Sci. 22, 361). It is remarkable that in Western Europe, as in the Caucasian population of North America, 12-15% are homozygotic carriers of the -786-variant, that is to say they have the genotype .sup.-786C/C. Approximately 48% are heterozygotic for this SNP, that is to say, they have the genotype .sup.-786C/T, and approximately 38% are homozygotic carriers of the .sup.-786T-variant, that is to say, they have the genotype .sup.-786T/T. It is also interesting that this mutation evidently does not occur in other mammals (dog, mouse, rat and cattle), because a base is missing at the corresponding position in the eNOS promoter in these species.

At page 14, lines 1-17, replace the paragraph with the following:

The present invention therefore relates to the provision of a decoy oligonucleotide, which is capable of binding in a sequence-specific manner to a protein or a protein complex (referred to below as "transcription factor" or "inhibitory transcription factor". The sequence of a decoy oligonucleotide, which is used to prevent the binding of the inhibitory transcription factor, is the sequence, to which the transcription factor binds in the promoter of the eNOS gene. The cis-element decoy according to the invention provides the following 10-mer consensus core-binding sequence: 5'-CTBBCYGBCT-3' (SEQ ID NO: 33) wherein Y=C or T and B=C,G or T. The cis-element decoy can, furthermore, be larger than the 10-mer core-binding sequence and can be extended at the 5'-end and/or at the 3'-end. Corresponding mutations in the region of the core-binding sequence (e.g. 5'-CTAGCTGACT-3' (SEQ ID NO:65)) lead to a complete loss of the

binding of the transcription factor to the decoy oligonucleotide, evident from the absence of biological effect (Table 3).